Warmer and drier ecosystems select for smaller bacterial genomes in global soils

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Introduction / Results

Genome size is fundamental for the prediction of microbial physiology, their ecological relationships with other microbes and the environment and their evolutionary histories. This is because

(i) genome size is linked to other bacterial traits related to life history strategies, e.g., growth rate and tolerance to extreme conditions;

(ii) variation in genome size among microbial taxa can reflect evolutionary events such as genome expansion and reduction that may be associated with emerging of new species, functions or lifestyles;

(iii) organisms with large genomes require more resources to grow and reproduce and can have a more restricted ecological distribution (large genome constraint hypothesis).

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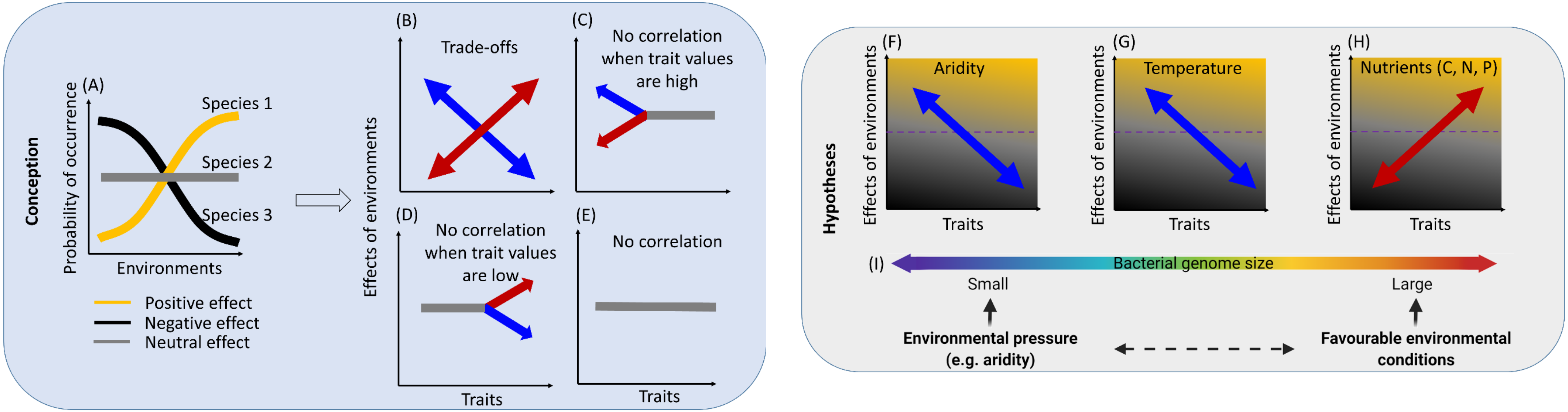

Conception and hypotheses: The ecological responses of the probabilities of bacterial occurrences to environmental gradients.

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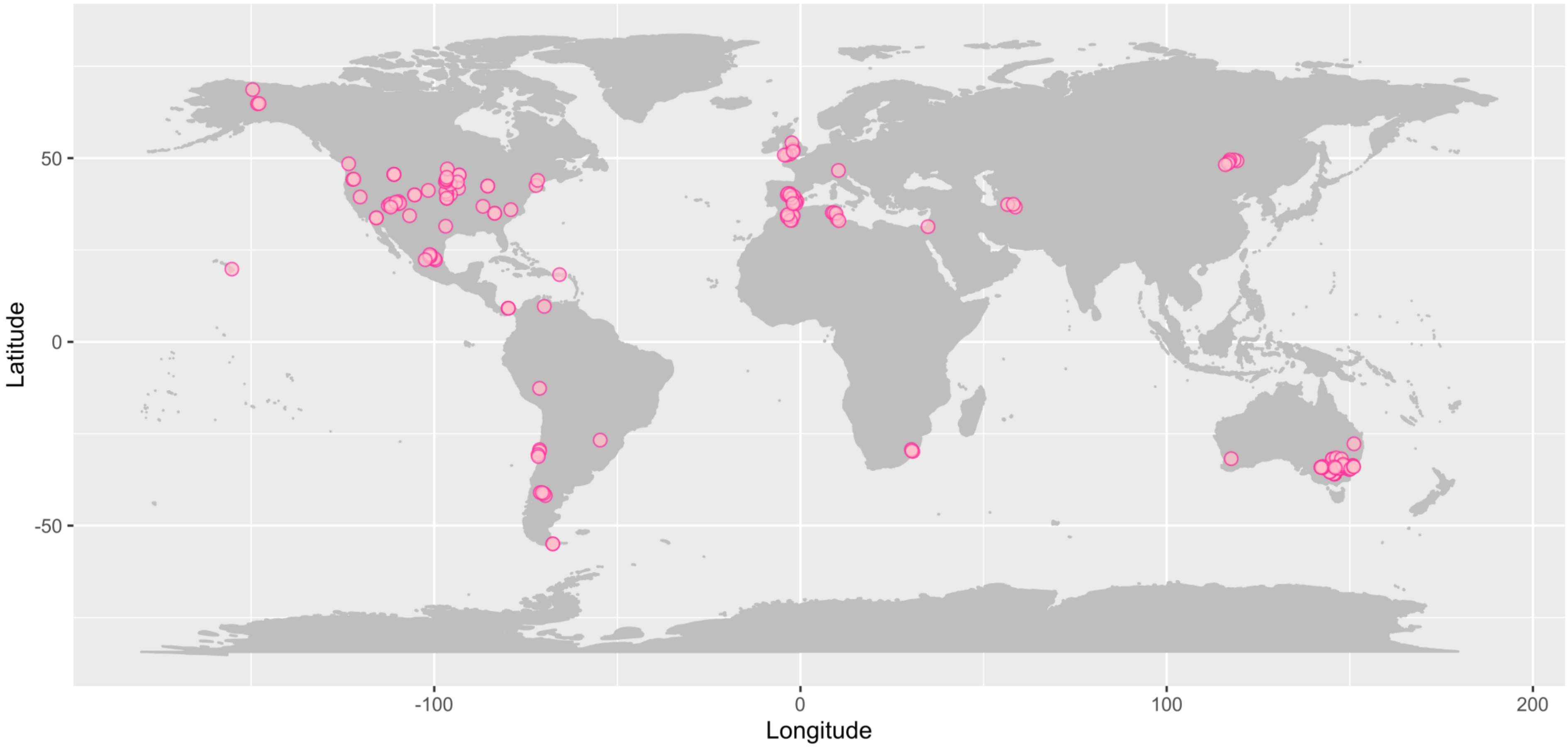

A map summarising sampling locations of the 237 samples across the globe. Each dot represents a sampling location.

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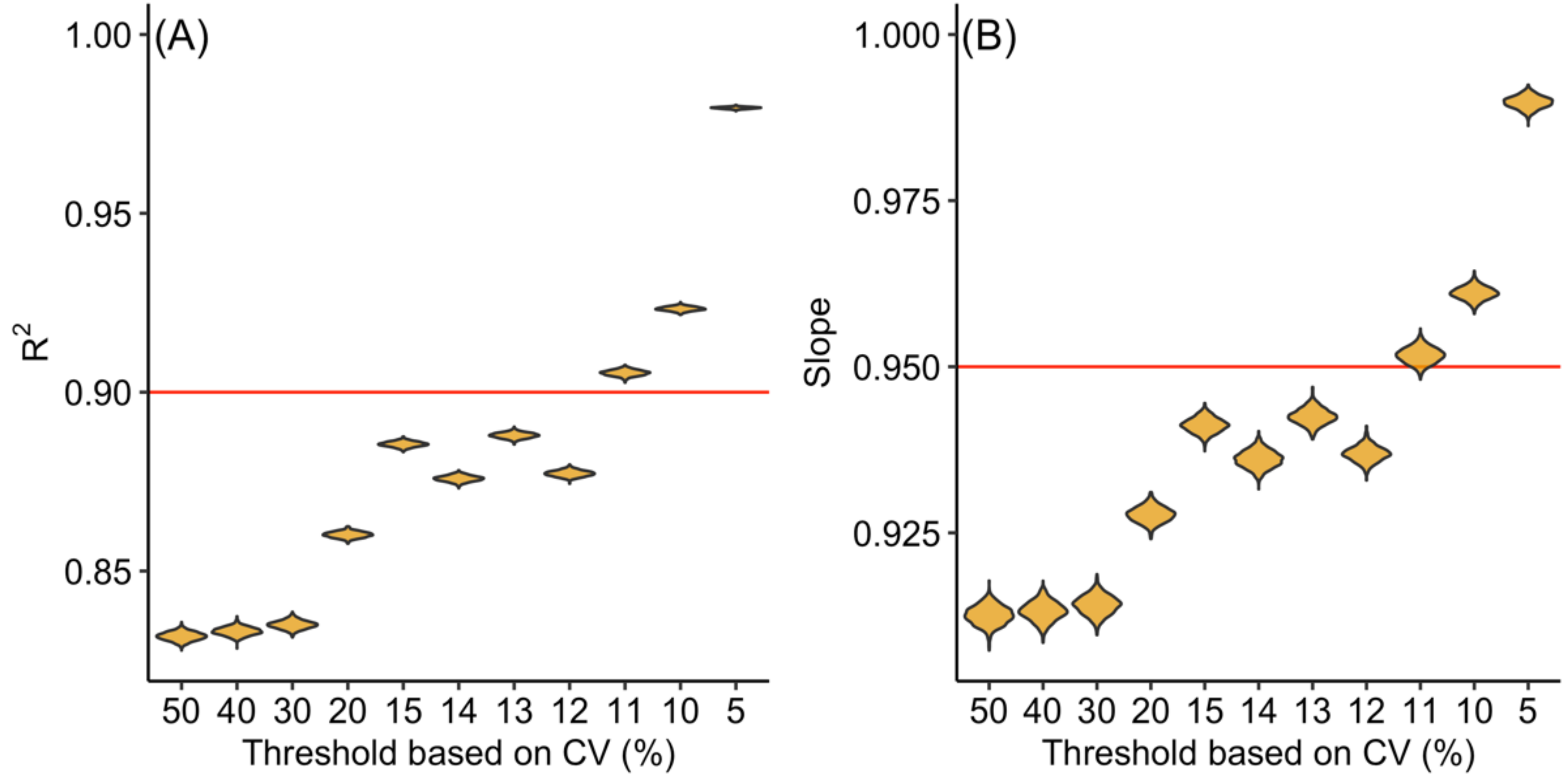

Violin plots demonstrate R^2 extracted from the correlation between predicted genome size and true genome size value at the species level for each threshold that was used to filter the bacterial genera.

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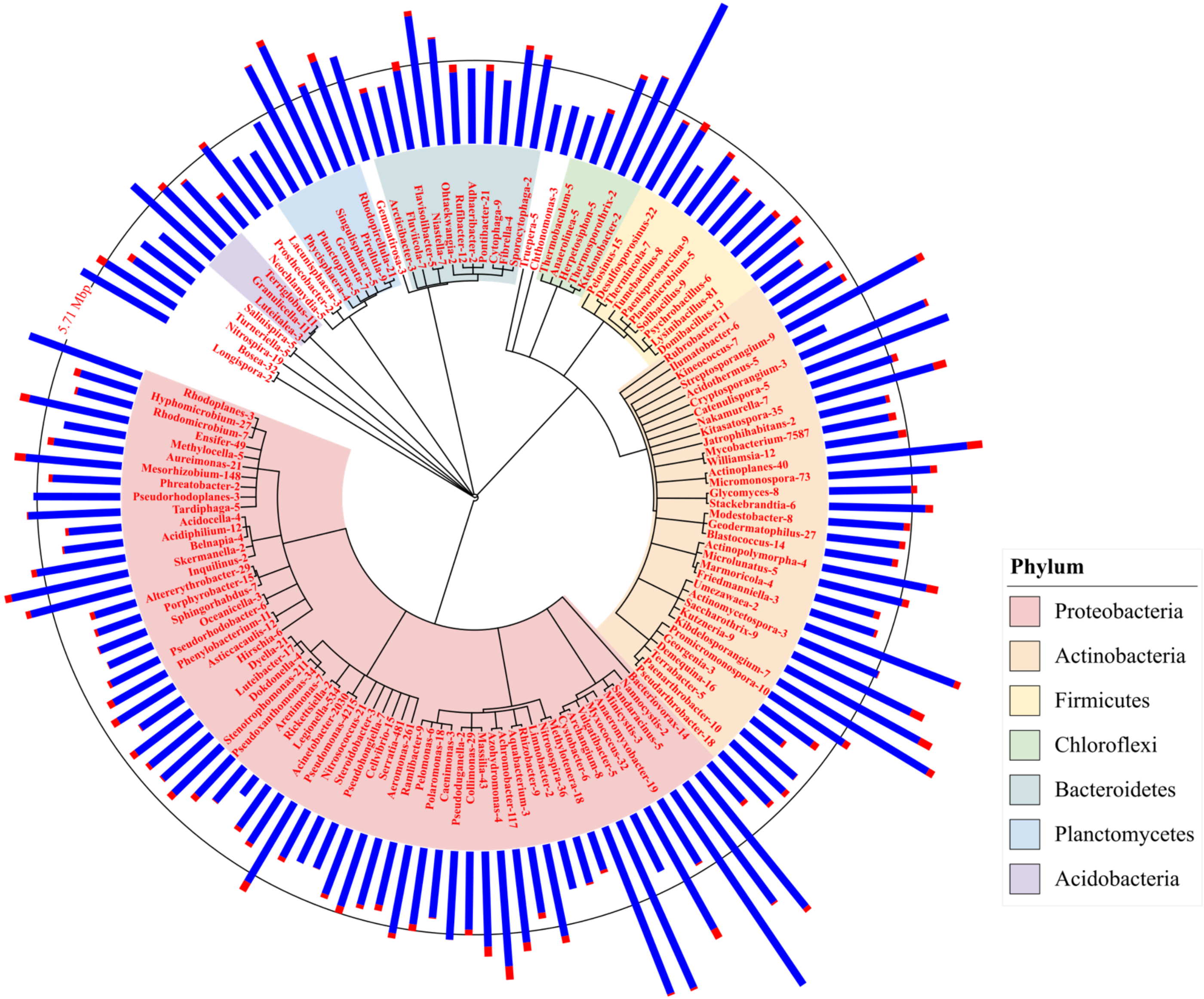

Phylogenetic tree with terminal branches for the studied bacteria genus. Blue bars show the genome size for each genus. Red bars represent standard deviation (SD) of genome size of that genus. The number of available genomes of a specific genus is labelled beside its name. The black circle line indicates the mean genome size averaged for all genera, which is 5.71 Mbp.

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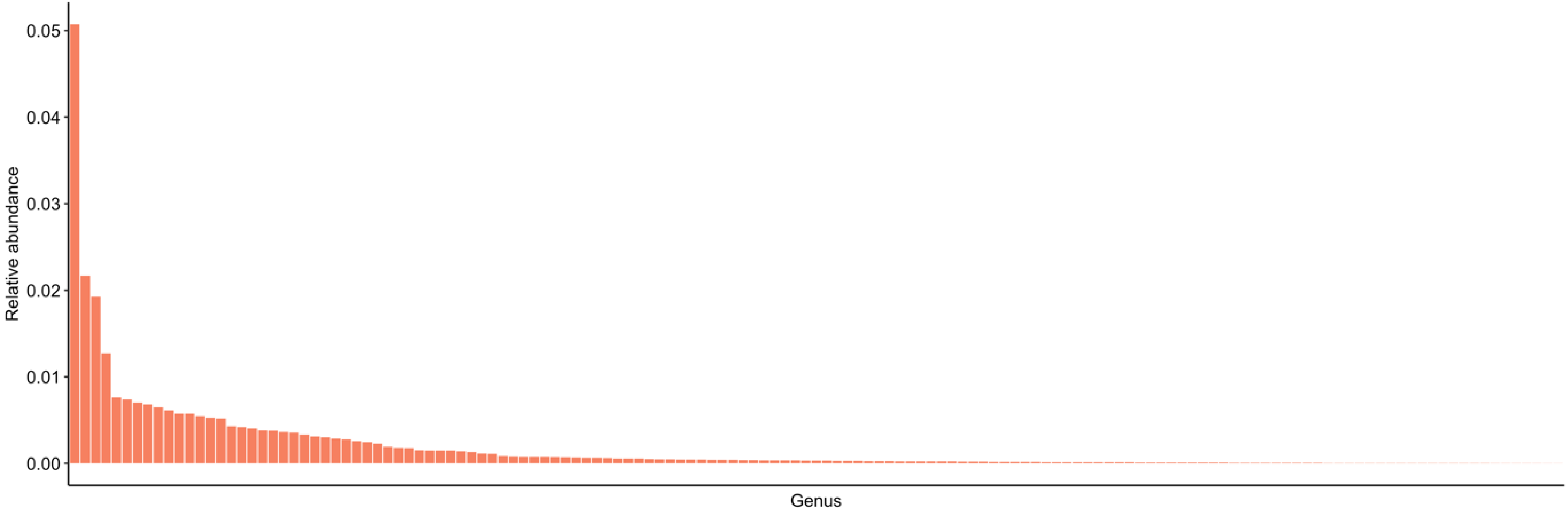

The relative abundance of each of the bacterial genera included in the joint species distribution model.

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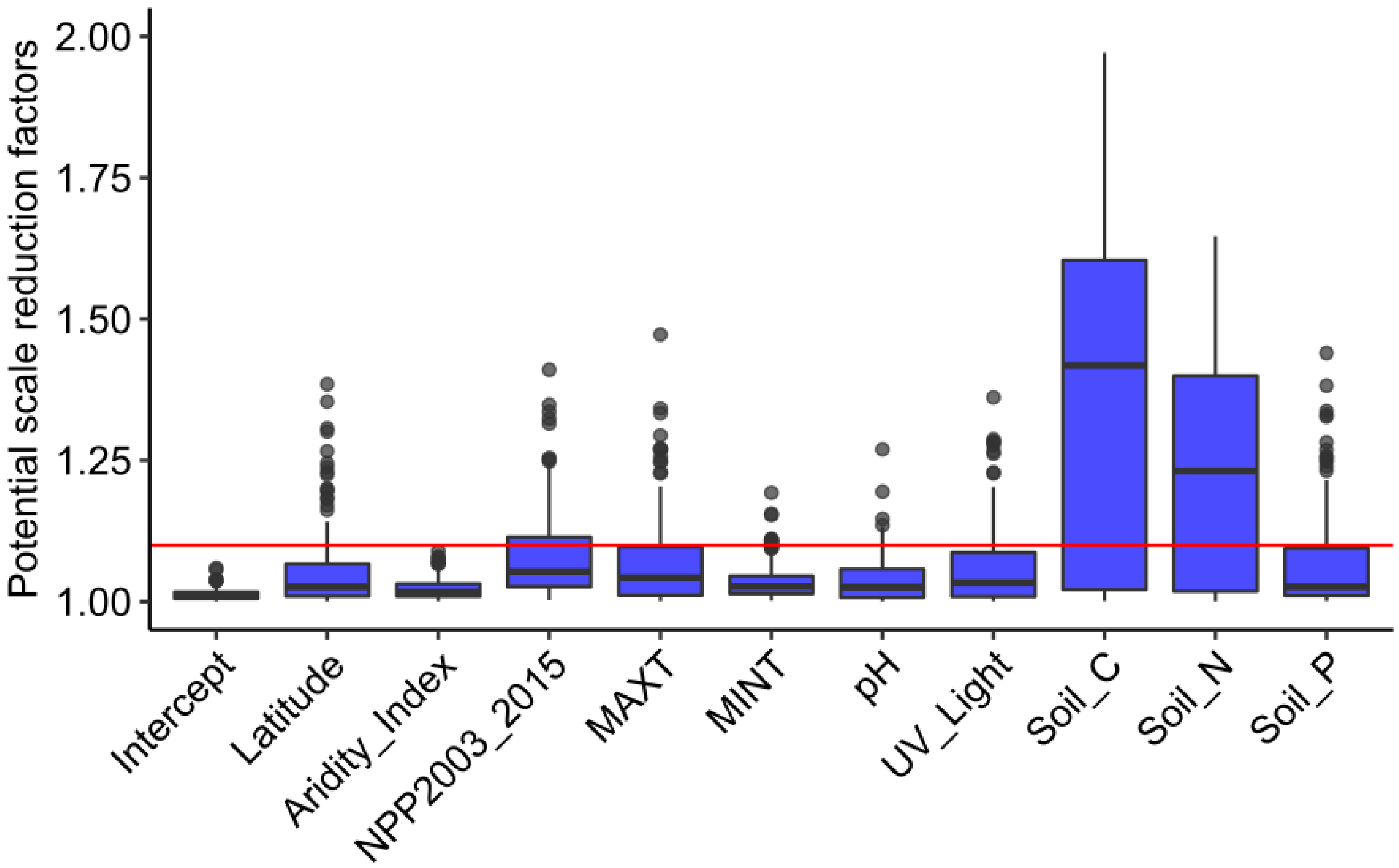

Markov Chain Monte Carlo (MCMC) convergence statistics after the Hierarchical Modelling of Species Communities (HMSC) fitting, measured as potential scale reduction factors.

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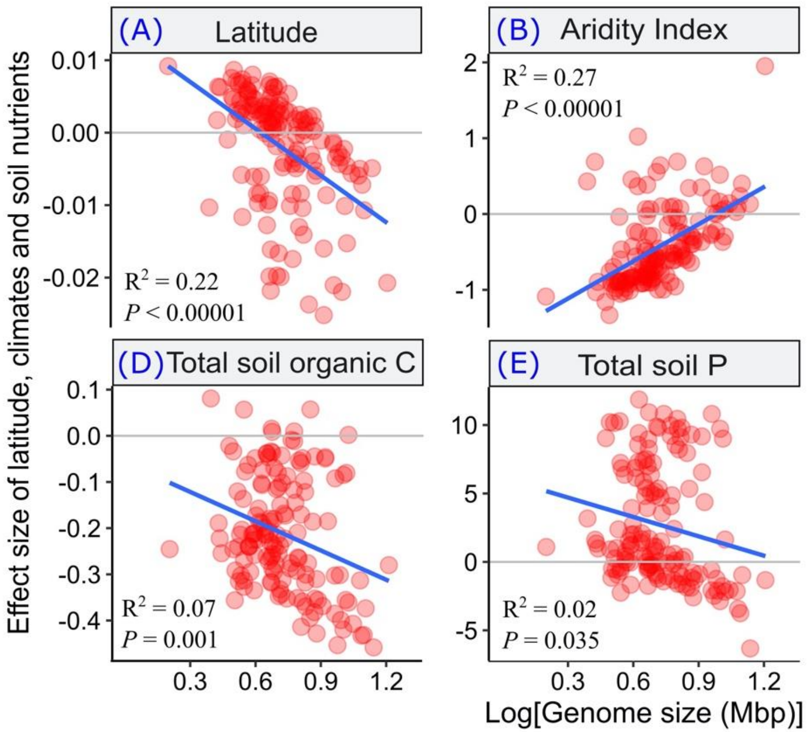

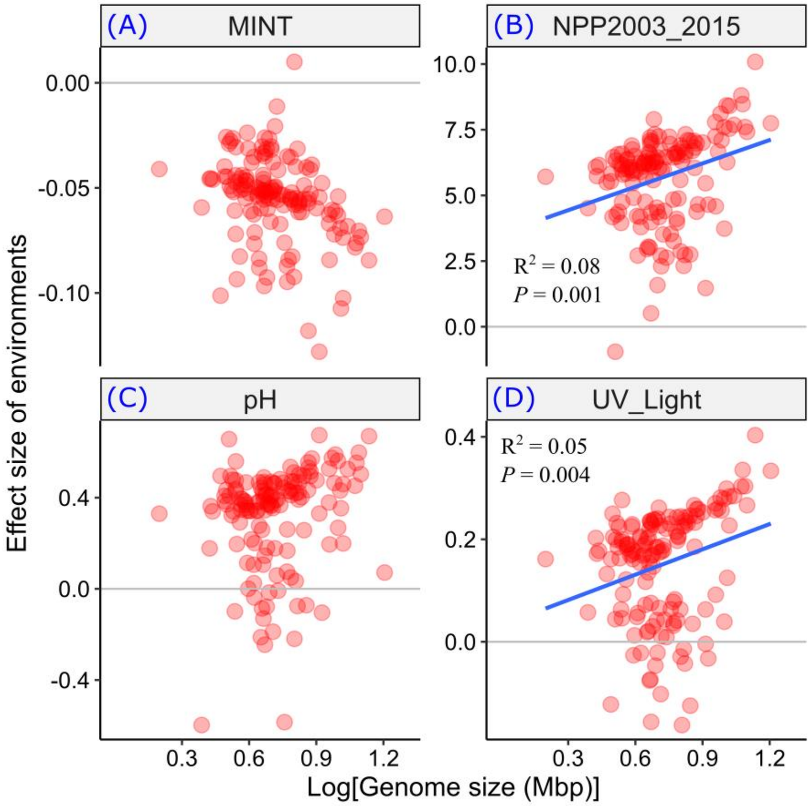

Correlations between bacterial genome size (log-transformed; Mbp) and the effects of environmental conditions on bacterial occurrence. Y axis indicates effect sizes of an environmental condition, which are slopes (beta-parameters) of the relationship between bacterial occurrence probability and environmental conditions, calculated from the Hierarchical Modelling of Species Communities (HMSC).

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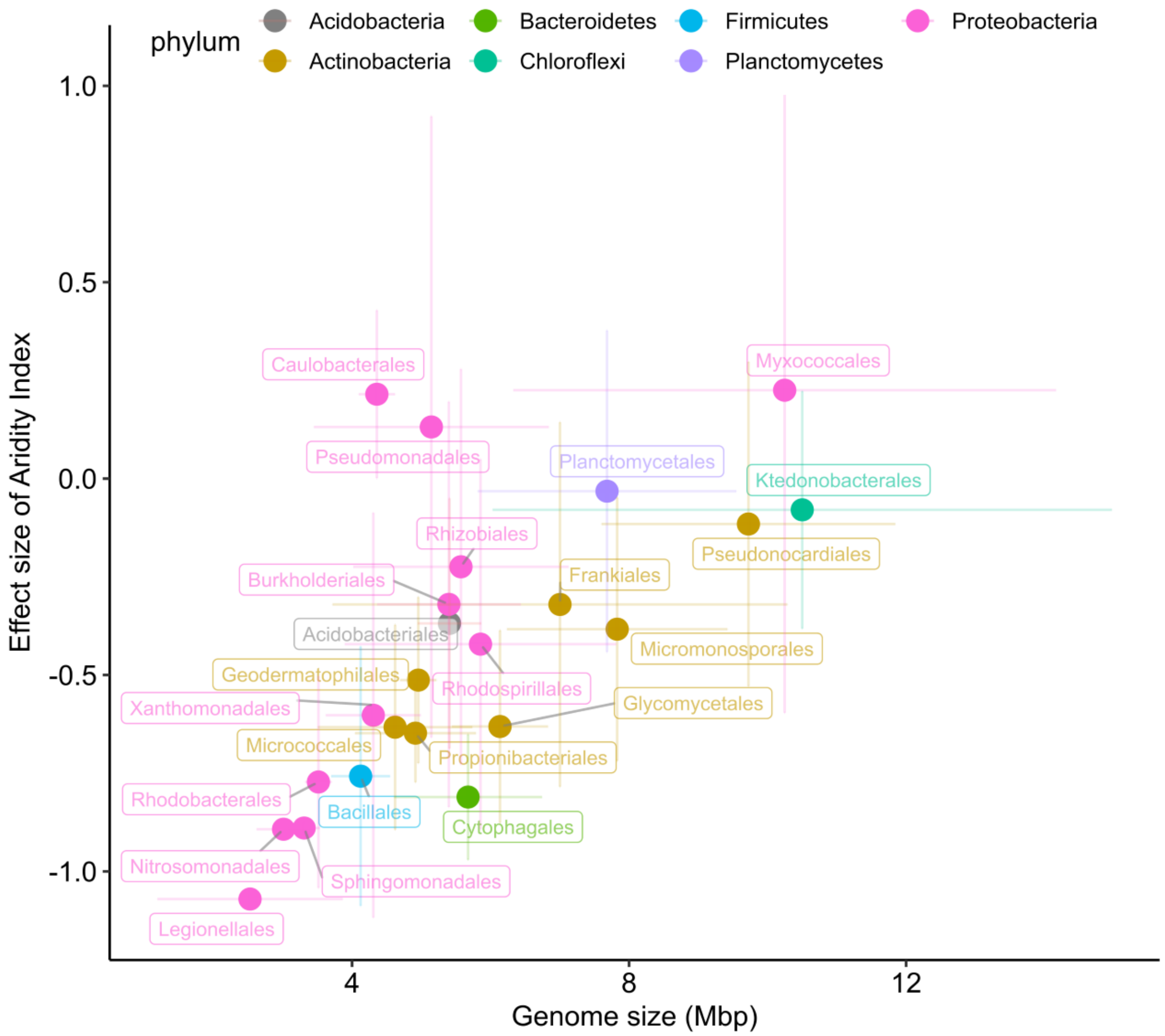

Distribution of effect size of aridity index against bacterial genome size at the bacterial order level.

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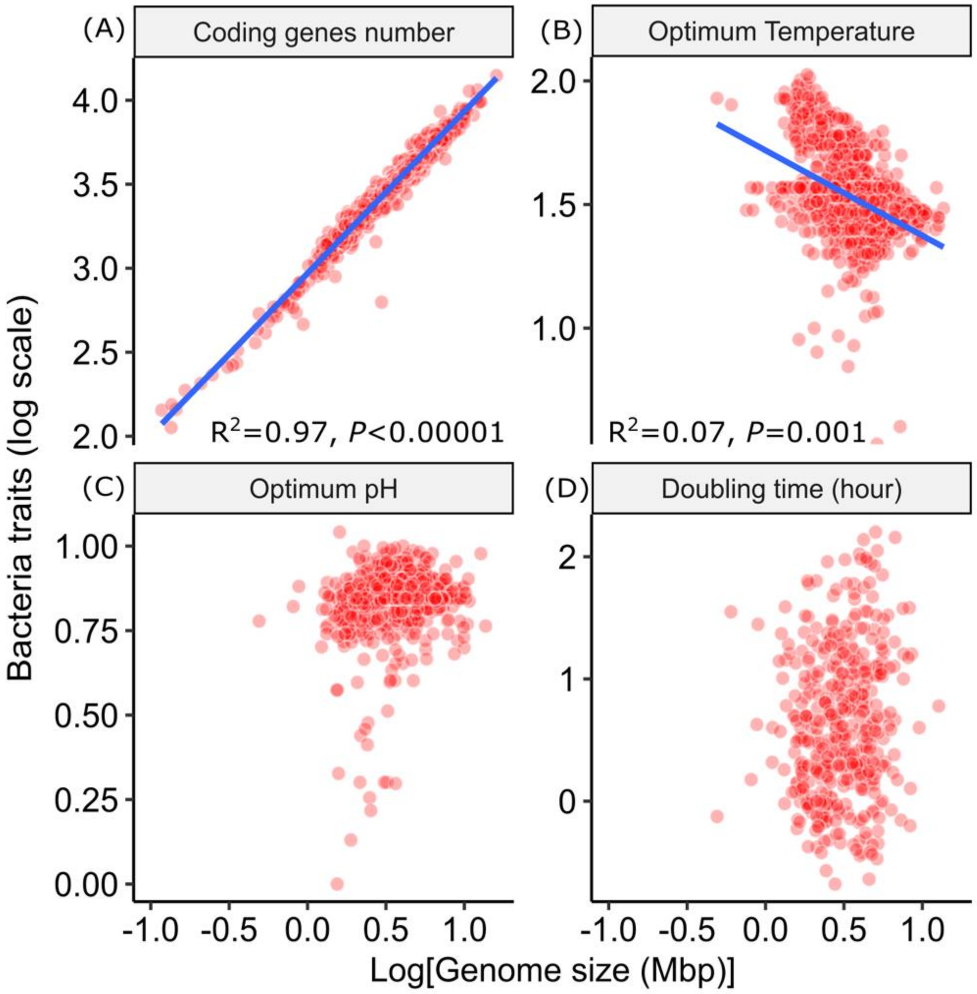

Correlations between genome size (log-transformed; Mbp) and bacteria traits at the genus level. The traits included coding gene number (A), optimum temperature (B), optimum pH (C) and bacteria doubling time that indicates bacterial growth rate (D).

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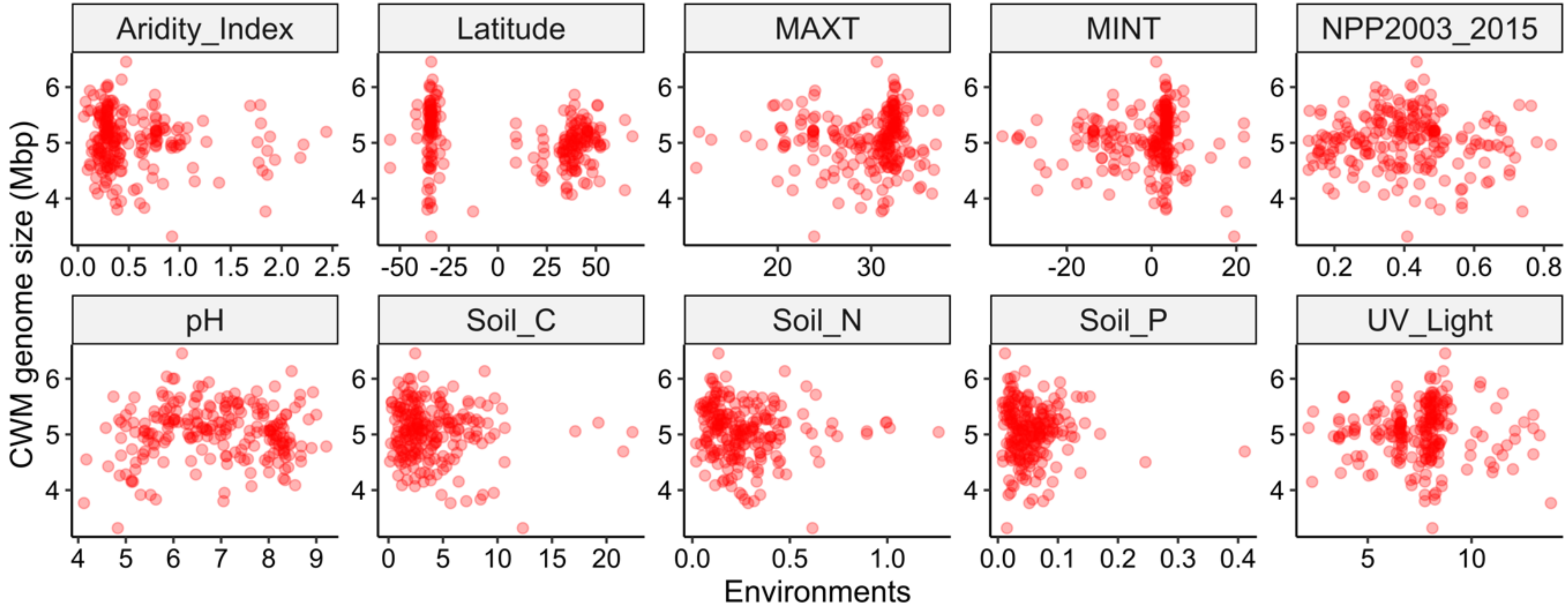

Community weighted mean (CWM) for bacterial genome size in soil relative to environmental variables.

Summary

- Overall, our study provides novel evidence that environmental stress associated with increases in aridity and warmer climates favours bacteria with smaller genomes in soils.
- Despite the unknown consequences of such microbial changes to ecosystem functions, future climate change research and policy-making should consider soil bacteria and their functional traits as they play important roles in soil carbon sequestration and maintaining ecosystem functions.
- Our study also suggests that lower soil fertility (soil C and P) and higher UV light level favour bacteria with larger genomes, which can dominate in soils where resources are scarce but without major restrictions on slow growth bacteria.
- Future research is warranted to validify our findings by investigating bacterial community assembly in soil and other ecosystems by determining genome size from metagenomes across environmental gradients.

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